



SEQUENCE LISTING

RECEIVED
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TECH CENTER 1600/2900

<110> Mahajan, Pramod
Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and its
Uses

<130> 5718-34

<140> US 09/236,995

<141> 1999-01-26

<150> US 60/072,785

<151> 1998-01-27

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<170> FastSEQ for Windows Version 4.0

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<221> misc_feature

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Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
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cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

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aca	gct	gct	cct	cct	gag	aaa	tgt	aca	att	gag	att	gct	cca	tct	gcc	336	
Thr	Ala	Ala	Pro	Pro	Glu	Lys	Cys	Thr	Ile	Glu	Ile	Ala	Pro	Ser	Ala		
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Arg	Thr	Ser	Cys	Arg	Arg	Cys	Ser	Glu	Lys	Ile	Thr	Lys	Gly	Ser	Val		
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Arg	Leu	Ser	Ala	Lys	Leu	Glu	Ser	Glu	Gly	Pro	Lys	Gly	Ile	Pro	Trp		
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Tyr	His	Ala	Asn	Cys	Phe	Phe	Glu	Val	Ser	Pro	Ser	Ala	Thr	Val	Glu		
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Lys	Phe	Ser	Gly	Trp	Asp	Thr	Leu	Ser	Asp	Glu	Asp	Lys	Arg	Thr	Met		
			165						170					175			
ctc	gat	ctt	gtt	aaa	aaa	gat	gtt	ggc	aac	aat	gaa	caa	aat	aag	ggc	576	
Leu	Asp	Leu	Val	Lys	Lys	Asp	Val	Gly	Asn	Asn	Glu	Gln	Asn	Lys	Gly		
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Ser	Lys	Arg	Lys	Lys	Ser	Glu	Asn	Asp	Ile	Asp	Ser	Tyr	Lys	Ser	Ala		
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agg	tta	gat	gaa	agt	aca	tct	gaa	ggc	aca	gtg	cga	aac	aaa	ggg	caa	672	
Arg	Leu	Asp	Glu	Ser	Thr	Ser	Glu	Gly	Thr	Val	Arg	Asn	Lys	Gly	Gln		
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ctt	gta	gac	cca	cgt	ggc	tcc	aat	act	agt	tca	gct	gat	atc	caa	cta	720	
Leu	Val	Asp	Pro	Arg	Gly	Ser	Asn	Thr	Ser	Ser	Ala	Asp	Ile	Gln	Leu		
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aag	ctt	aag	gag	caa	agt	gac	aca	ctt	tgg	aag	tta	aag	gat	gga	ctt	768	
Lys	Leu	Lys	Glu	Gln	Ser	Asp	Thr	Leu	Trp	Lys	Leu	Lys	Asp	Gly	Leu		
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Lys	Thr	His	Val	Ser	Ala	Ala	Glu	Leu	Arg	Asp	Met	Leu	Glu	Ala	Asn		
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Gly	Gln	Asp	Thr	Ser	Gly	Pro	Glu	Arg	His	Leu	Leu	Asp	Arg	Cys	Ala		
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gat	gga	atg	cta	ttt	gga	gcg	ctg	ggc	cct	tgc	cca	gtc	tgt	gct	aat	912	
Asp	Gly	Met	Leu	Phe	Gly	Ala	Leu	Gly	Pro	Cys	Pro	Val	Cys	Ala	Asn		
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Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser	
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Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys	
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Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys	
340 345 350	
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Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro	
355 360 365	
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Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu	
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Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln	
385 390 395 400	
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Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly	
405 410 415	
gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca	1296
Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala	
420 425 430	
tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg	1344
Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg	
435 440 445	
ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa	1392
Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys	
450 455 460	
aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag	1440
Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu	
465 470 475 480	
tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt gct	1488
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala	
485 490 495	
tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra	1536
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa	
500 505 510	
gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn	1584
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa	
515 520 525	
cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat	1632

His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
 530 535 540

gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt 1680
 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
 545 550 555 560

gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca 1728
 Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
 565 570 575

atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg 1776
 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
 580 585 590

gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt 1824
 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
 595 600 605

tac cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aaa 1872
 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
 610 615 620

gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc 1920
 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
 625 630 635 640

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 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
 645 650 655

ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra 2016
 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
 660 665 670

aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt 2064
 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
 675 680 685

gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg 2112
 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
 690 695 700

ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc 2160
 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
 705 710 715 720

ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt 2208
 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
 725 730 735

gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat 2256
 Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
 740 745 750

agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt 2304

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Asp	Ile	Thr	Pro	Leu	Ala	His	Asp	Ser	Glu	Asp	Tyr	Lys	Leu	Ile	Glu	
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cag	tat	ctc	ctc	aac	aca	cat	gct	cct	act	cac	aag	gac	tgg	tcg	ctg	2400
Gln	Tyr	Leu	Leu	Asn	Thr	His	Ala	Pro	Thr	His	Lys	Asp	Trp	Ser	Leu	
	785				790				795						800	
gaa	ctg	gag	gaa	gtt	ttt	tca	ctt	gat	cga	gat	gga	gaa	ctt	aat	aag	2448
Glu	Leu	Glu	Glu	Val	Phe	Ser	Leu	Asp	Arg	Asp	Gly	Glu	Leu	Asn	Lys	
				805					810						815	
tac	tca	aga	tat	aaa	aat	aat	ctg	cat	aac	aag	atg	cta	tta	tgg	cac	2496
Tyr	Ser	Arg	Tyr	Lys	Asn	Asn	Leu	His	Asn	Lys	Met	Leu	Leu	Trp	His	
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Gly	Ser	Arg	Leu	Thr	Asn	Phe	Val	Gly	Ile	Leu	Ser	Gln	Gly	Leu	Arg	
		835					840					845				
att	gca	cct	cct	gag	gca	cct	gtt	act	ggc	tat	atg	ttc	ggc	aaa	ggc	2592
Ile	Ala	Pro	Pro	Glu	Ala	Pro	Val	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly	
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Leu	Tyr	Phe	Ala	Asp	Leu	Val	Ser	Lys	Ser	Ala	Gln	Tyr	Cys	Tyr	Val	
	865				870					875					880	
gat	agg	aat	aat	cct	gta	ggt	ttg	atg	ctt	ctt	tct	gag	gtt	gct	tta	2688
Asp	Arg	Asn	Asn	Pro	Val	Gly	Leu	Met	Leu	Leu	Ser	Glu	Val	Ala	Leu	
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gga	gac	atg	tat	gaa	cta	aag	aaa	gcc	acg	tcc	atg	gac	aaa	cct	cca	2736
Gly	Asp	Met	Tyr	Glu	Leu	Lys	Lys	Ala	Thr	Ser	Met	Asp	Lys	Pro	Pro	
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aga	ggg	aag	cat	tcg	acc	aag	gga	tta	ggc	aaa	acc	gtg	cca	ctg	gag	2784
Arg	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Thr	Val	Pro	Leu	Glu	
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tca	gag	ttt	gtg	aag	tgg	agg	gat	gat	gtc	gta	gtt	ccc	tgc	ggc	aag	2832
Ser	Glu	Phe	Val	Lys	Trp	Arg	Asp	Asp	Val	Val	Val	Pro	Cys	Gly	Lys	
	930					935					940					
ccg	gtg	cca	tca	tca	att	agg	agc	tct	gaa	ctc	atg	tac	aat	gag	tac	2880
Pro	Val	Pro	Ser	Ser	Ile	Arg	Ser	Ser	Glu	Leu	Met	Tyr	Asn	Glu	Tyr	
	945				950					955				960		
atc	gtc	tac	aac	aca	tcc	cag	gtg	aag	atg	cag	ttc	ttg	ctg	aag	gtg	2928
Ile	Val	Tyr	Asn	Thr	Ser	Gln	Val	Lys	Met	Gln	Phe	Leu	Leu	Lys	Val	
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cgt	ttc	cat	cac	aag	agg	tag										2949

B1 Cont

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<213> Zea mays

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683, 684, 685, 686, 693, 699, 703, 706, 707, 708, 709, 710
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35 40 45
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
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Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80
Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
85 90 95
Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
100 105 110
Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
115 120 125
Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
130 135 140
Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
145 150 155 160
Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
165 170 175
Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
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Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
195 200 205
Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
210 215 220
Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
225 230 235 240
Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
245 250 255
Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
260 265 270
Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
275 280 285
Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
290 295 300
Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
305 310 315 320

Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335
 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350
 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 400
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
 405 410 415
 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
 420 425 430
 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
 435 440 445
 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
 450 455 460
 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
 465 470 475 480
 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
 485 490 495
 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
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 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
 515 520 525
 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
 530 535 540
 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
 545 550 555 560
 Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
 565 570 575
 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
 580 585 590
 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
 595 600 605
 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
 610 615 620
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 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
 645 650 655
 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
 660 665 670
 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
 675 680 685
 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
 690 695 700
 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
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 725 730 735
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 740 745 750
 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
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Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
 770 . 775 780
 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
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 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
 805 810 815
 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
 820 825 830
 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
 835 840 845
 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
 850 855 860
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 865 870 875 880
 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
 885 890 895
 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
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 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
 915 920 925
 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
 930 935 940
 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
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 Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
 20 25 30
 ggc tat atg ttc ggc aaa ggc ctc tac ttt gca gat cta gta agc aag 144
 Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
 35 40 45
 agc gca caa tac tgt tat gtg gat agg aat aat cct gta ggt ttg atg 192
 Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
 50 55 60

ctt ctt tct gag gtt gct tta gga gac atg tat gaa cta aag aaa gcc 240
 Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
 65 70 75 80
 acg tcc atg gac aaa cct cca aga ggg aag cat tcg acc aag gga tta 288
 Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
 85 90 95
 ggc aaa acc gtg cca ctg gag tca gag ttt gtg aag tgg agg gat gat 336
 Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
 100 105 110
 gtc gta gtt ccc tgc ggc aag ccg gtg cca tca tca att agg agc tct 384
 Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
 115 120 125
 gaa ctc atg tac aat gag tac atc gtc tac aac aca tcc cag gtg aag 432
 Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
 130 135 140
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 35 40 45
 Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
 50 55 60
 Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
 65 70 75 80
 Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
 85 90 95
 Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
 100 105 110
 Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
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<212> DNA
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